Resource Summary Report

Generated by RRID on Apr 19, 2025

CisGenome

RRID:SCR_001558
Type: Tool

Proper Citation

CisGenome (RRID:SCR_001558)

Resource Information

URL: http://www.biostat.jhsph.edu/~hji/cisgenome/index.htm

Proper Citation: CisGenome (RRID:SCR_001558)

Description: Integrated software tool for tiling array, ChIP-seq, genome and cis-regulatory element analysis.

Synonyms: CisGenome v2.0

Resource Type: data analysis tool

Defining Citation: PMID:18978777

Keywords: sequencing software, chip seq, downstream analysis, chip analysis, bio.tools

Funding:

Availability: Free, Non-commercial use

Resource Name: CisGenome

Resource ID: SCR_001558

Alternate IDs: OMICS_00423, biotools:cisgenome

Alternate URLs: https://bio.tools/cisgenome

Old URLs: http://biogibbs.stanford.edu/~jihk/CisGenome/index.htm

Record Creation Time: 20220129T080208+0000

Record Last Update: 20250410T064723+0000

Ratings and Alerts

No rating or validation information has been found for CisGenome.

No alerts have been found for CisGenome.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 80 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Itoh Y, et al. (2024) Analysis of the DNA-binding properties of TGF-?-activated Smad complexes unveils a possible molecular basis for cellular context-dependent signaling. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 38(15), e23877.

Hu K, et al. (2024) Mecp2 promotes the anti-inflammatory effect of alpinetin via epigenetic modification crosstalk. Journal of cellular and molecular medicine, 28(13), e18510.

Haghani V, et al. (2024) Improving rigor and reproducibility in chromatin immunoprecipitation assay data analysis workflows with Rocketchip. bioRxiv : the preprint server for biology.

Hosseinzadeh L, et al. (2024) The androgen receptor interacts with GATA3 to transcriptionally regulate a luminal epithelial cell phenotype in breast cancer. Genome biology, 25(1), 44.

Zhao M, et al. (2023) NF-?B subunits direct kinetically distinct transcriptional cascades in antigen receptor-activated B cells. Nature immunology, 24(9), 1552.

Fang Y, et al. (2023) DNA methylation entropy is associated with DNA sequence features and developmental epigenetic divergence. Nucleic acids research, 51(5), 2046.

Nagata K, et al. (2022) Runx2 and Runx3 differentially regulate articular chondrocytes during surgically induced osteoarthritis development. Nature communications, 13(1), 6187.

Marchal C, et al. (2022) Context-dependent CpG methylation directs cell-specific binding of transcription factor ZBTB38. Epigenetics, 17(13), 2122.

Lui JC, et al. (2022) A neomorphic variant in SP7 alters sequence specificity and causes a

high-turnover bone disorder. Nature communications, 13(1), 700.

Liao CG, et al. (2022) Active demethylation upregulates CD147 expression promoting non-small cell lung cancer invasion and metastasis. Oncogene, 41(12), 1780.

Hojo H, et al. (2022) Runx2 regulates chromatin accessibility to direct the osteoblast program at neonatal stages. Cell reports, 40(10), 111315.

Lex RK, et al. (2022) GLI transcriptional repression is inert prior to Hedgehog pathway activation. Nature communications, 13(1), 808.

Li J, et al. (2021) Mechanism of forkhead transcription factors binding to a novel palindromic DNA site. Nucleic acids research, 49(6), 3573.

Shin HM, et al. (2021) Chromatin accessibility of circulating CD8+ T cells predicts treatment response to PD-1 blockade in patients with gastric cancer. Nature communications, 12(1), 975.

Kanazawa S, et al. (2021) Mesenchymal stromal cells in the bone marrow niche consist of multi-populations with distinct transcriptional and epigenetic properties. Scientific reports, 11(1), 15811.

Pei J, et al. (2021) Multi-omics integration identifies key upstream regulators of pathomechanisms in hypertrophic cardiomyopathy due to truncating MYBPC3 mutations. Clinical epigenetics, 13(1), 61.

Pei J, et al. (2020) H3K27ac acetylome signatures reveal the epigenomic reorganization in remodeled non-failing human hearts. Clinical epigenetics, 12(1), 106.

Doskey CM, et al. (2020) 2,3,7,8-Tetrachlorodibenzo-p-dioxin (TCDD) alters hepatic polyunsaturated fatty acid metabolism and eicosanoid biosynthesis in female Sprague-Dawley rats. Toxicology and applied pharmacology, 398, 115034.

Jeon H, et al. (2020) Comparative analysis of commonly used peak calling programs for ChIP-Seq analysis. Genomics & informatics, 18(4), e42.

Ji Z, et al. (2020) Single-cell ATAC-seq signal extraction and enhancement with SCATE. Genome biology, 21(1), 161.